STIC Biotechnology Systems Branch

/ FWO

CRF Problem Report

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: _10/554,238_
Filing Date: _10/20/05_
Date Processed by STIC: _2/23/07_

STIC Contact: **Mark Spencer: Telephone: 571-272-2510; Fax: 571-273-0221**

Nature of CRF Problem:

_____ (circle one) Damaged or Unreadable (for Unreadable, see attached)
_____ Blank (no files on CRF) (see attached)
_____ Empty file (filename present, but no bytes in file) (see attached)
_____ Wrong file saved to CRF (invention title, docket number, or applicant(s) do not
          match those in official application)   (see attached)
_____ Not saved in ASCII text
_____ Sequence Listing was embedded in the file. According to Sequence Rules,
          submitted file should **only** be the Sequence Listing.
_____ Did not contain a Sequence Listing. (see attached sample)
___✓__ Other:
  Sequence listing was split into separate files .

**PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM TO REDUCE ERRORS.
SEE BELOW FOR ADDRESS:**
          http:/www.uspto.gov/web/offices/pac/checker/chkrnote.htm

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
    User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
    U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
    Alexandria, VA 22314

Revised 01/20/06

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/554,238_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
____Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
                         prevent "wrapping."

2____Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
____Numbering   use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
____"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
____(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                         (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                         (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                         This sequence is intentionally skipped
                         Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
____(NEW RULES)   <210> sequence id number
                         <400> sequence id number
                         000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
____(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
____Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
____"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

SEQUENCE LISTING ⟵ *do NOT use bold font* 2

Per 1.823
of Sequence
Rules,

use a
fixed-width
font

<110> Breitenstein, Antje

<120> Method for the Detection of Bacteria of the Genus Legionella

<140> US 10/554,238

<141> 2005-10-20

<160> 8

<210> 1
<211> 19
<212> DNA
<213> Legionella pneumophila
<400> 1
<400> ttcgccgccc tctgtatcg

19 ⟵ *insert cumulative*
base total at
right margin of each line

<210> 2
<211> 18
<212> DNA
<213> Legionella pneumophila
<400> 2
<400> atctgaccgt cccaggtt

18 ⟵

<210> 3
<211> 20
<212> DNA
<213> Legionella feelei
<400> 3
<400> gcgccactaa cctcattcat

20 ⟵

<210> 4
<211> 20
<212> DNA
<213> Legionella feelei
<400> 4
<400> tatacaacca cctacgcacc

20 ⟵

please re-arrange <400> line as shown. It does NOT appear on same line as bases or amino acids

The above was one of the non-ASCII files on submitted disk

"Sequence Listing 1.DOC"

(see item 4 on Error summary sheet)

see next page

```
<210> 5
<211> 20
<212> DNA
<213> Legionella jordanis
<400> 5
<400> cttacggtcc ccagctttt          20
```

```
<210> 6
<211> 20
<212> DNA
<213> Legionella jordanis
<400> 6
<400> ccactcctcc ccactgaaag          20
```

```
<210> 7
<211> 19
<212> DNA
<213> Legionella sp.
<400> 7
<400> cctcctcccc actgaaagt          19
```

```
<210> 8
<211> 20
<212> DNA
<213> Legionella sp.
<400> 8
<400> cactgtatgt caagggtagg          20
```

The above was the other file on submitted disk "Sequence Listing 2. DOC"

DO NOT split a sequence listing file.

Per 1.824 of Sequence Rules the sequence listing must be one file on submitted computer readable form

Please consult Sequence Rules for valid format